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10 August 2021 (Tuesday), 3.30pm
Hosted by: Dr Naweed Naqvi

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Molecular innovations in rebuilding a cellular load-bearing machine

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Cryptococcus neoformans is a dreaded fungal pathogen that causes pneumonia and fungal meningitis primarily in immunocompromised individuals. C. neoformans is a basidiomycete yeast. Since aneuploidy is a major cause of drug resistance in C. neoformans, we have been studying its centromere-kinetochore complex that aids chromosome segregation. C. neoformans possesses long regional centromeres rich in various classes of retrotransposons. The microtubule-binding outer kinetochore is coupled to centromeric chromatin through CENP-CMif2, CENP-TCnn1, and CENP-UAme1 linker pathways originating from the constitutive centromere associated network (CCAN) of the inner kinetochore. We demonstrate the recurrent loss of most CCAN components, including certain kinetochore linkers during the evolution of the fungal phylum of Basidiomycota. By kinetochore interactome analyses in C. neoformans, a model basidiomycete, a forkhead-associated domain containing protein "bridgin" was identified as a kinetochore component along with other predicted kinetochore proteins. In vivo and in vitro functional analyses of bridgin reveal its ability to connect the outer kinetochore with centromeric chromatin to ensure accurate chromosome segregation. Unlike established CCAN-based linkers, bridgin is recruited at the outer kinetochore establishing its role as a distinct family of kinetochore proteins. Presence of bridgin homologs in non-fungal lineages suggests an ancient divergent strategy exists to bridge the outer kinetochore with centromeric chromatin.

Kaustuv Sanyal obtained Master of Science in Biotechnology from Madurai Kamaraj University, the PhD degree from Bose Institute (Kolkata) and a postdoctoral fellowship at the University of California, Santa Barbara, USA. He is professor in Molecular Biology and Genetics Unit at the JN Centre for Advanced Scientific Research. The major focus of his research is to understand the mechanism of chromosome segregation using various yeasts, both pathogenic and non-pathogenic, as model systems. He is also interested in the mechanism of genome indexing in unicellular organisms by histone variants and had contributed significantly in these research areas by publishing several papers and reviews.

Recent Publications:

1. Sreekumar L, Kumari K, Guin K, Bakshi A, Varshney N, Thimmappa BC, Narlikar L, Padinhateeri R, Siddharthan R, **Sanyal K** (2021) **Genome Research** 31:607- 621.

2. Sridhar S, Hori T, Nakagawa R, Fukagawa T, **Sanyal K** (2021) **Nature Communications** 12: 146.

3. Guin K, Chen Y, Mishra R, Muzaki SRBM, Thimmappa BC, O'Brien C, Butler G, Sanyal A, **Sanyal K** (2020) **eLife** 9: e58556.